

#6



PCT10

**RAW SEQUENCE LISTING**  
**PATENT APPLICATION:** US/10/030,271

**DATE:** 08/21/2002  
**TIME:** 15:44:48

**Input Set :** A:\217860US.ST25.txt  
**Output Set:** N:\CRF4\08212002\J030271.raw

3 <110> APPLICANT: OTA, TOSHIO  
 4 ISOGAI, TAKAO  
 5 NISHIKAWA, TETSUO  
 6 HIO, YURI  
 7 MIYOSHI, SOUSUKE  
 8 SATOH, SUSUMU  
 10 <120> TITLE OF INVENTION: APOPTOSIS-ASSOCIATED FACTOR  
 12 <130> FILE REFERENCE: 217860US0PCT  
 C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/030,271  
 C--> 15 <141> CURRENT FILING DATE: 2002-06-28  
 17 <150> PRIOR APPLICATION NUMBER: JP 11-194179  
 18 <151> PRIOR FILING DATE: 1999-07-08  
 20 <150> PRIOR APPLICATION NUMBER: US 60/159,586  
 21 <151> PRIOR FILING DATE: 1999-10-18  
 23 <160> NUMBER OF SEQ ID NOS: 13  
 25 <170> SOFTWARE: PatentIn version 3.1  
 27 <210> SEQ ID NO: 1  
 28 <211> LENGTH: 909  
 29 <212> TYPE: DNA  
 30 <213> ORGANISM: Homo sapiens  
 32 <220> FEATURE:  
 33 <221> NAME/KEY: CDS  
 34 <222> LOCATION: (1)..(909)  
 35 <223> OTHER INFORMATION:  
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 43 tgc ctg gac tac tac ggg atg ctg tcg ctt cac cgt atg ttc gag gtg 96  
 44 Cys Leu Asp Tyr Tyr Gly Met Leu Ser Leu His Arg Met Phe Glu Val  
 45 20 25 30  
 47 gtg ggc ggg caa ctg acc gag tgc gag ctg gag ctc ctg gcc ttt ctg 144  
 48 Val Gly Gly Gln Leu Thr Glu Cys Glu Leu Glu Leu Ala Phe Leu  
 49 35 40 45  
 51 ctg gat gag gct cct ggc gcc gga ggc tta gcc cgg gcc cgc agc 192  
 52 Leu Asp Glu Ala Pro Gly Ala Ala Gly Gly Leu Ala Arg Ala Arg Ser  
 53 50 55 60  
 55 ggc cta gag ctc ctg gag ctg gag cgc cgc ggg cag tgc ggc gag 240  
 56 Gly Leu Glu Leu Leu Glu Leu Glu Arg Arg Gly Gln Cys Gly Glu  
 57 65 70 75 80  
 59 agc aac ctg cgg ctg ctg ggg caa ctc ctg cgc gtg ctg gcc cgc cac 288  
 60 Ser Asn Leu Arg Leu Leu Gly Gln Leu Leu Arg Val Leu Ala Arg His  
 61 85 90 95

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63 gac ctg ctg ccg cac ctg gcg cgc aag cgg cgc cgg cca gtg tct cca	336
64 Asp Leu Leu Pro His Leu Ala Arg Lys Arg Arg Arg Pro Val Ser Pro	
65 100 105 110	
67 gaa cgc tat agc tat ggc acc tcc agc tct tca aag agg aca gag ggt	384
68 Glu Arg Tyr Ser Tyr Gly Thr Ser Ser Ser Lys Arg Thr Glu Gly	
69 115 120 125	
71 agc tgc cgt cgc cgt cgg cag tca agc agt tct gca aat tct cag cag	432
72 Ser Cys Arg Arg Arg Gln Ser Ser Ser Ala Asn Ser Gln Gln	
73 130 135 140	
75 ggt cag tgg gag aca ggc tcc ccc cca acc aag cgg cag cgg cgg agt	480
76 Gly Gln Trp Glu Thr Gly Ser Pro Pro Thr Lys Arg Gln Arg Arg Ser	
77 145 150 155 160	
79 cgg ggc cgg ccc agt ggt ggt gcc aga cgg cgg cgg aga ggg gcc cca	528
80 Arg Gly Arg Pro Ser Gly Gly Ala Arg Arg Arg Arg Gly Ala Pro	
81 165 170 175	
83 gcc gca ccc cag cag cag tca gag ccc gcc aga cct tcc tct gaa ggc	576
84 Ala Ala Pro Gln Gln Ser Glu Pro Ala Arg Pro Ser Ser Glu Gly	
85 180 185 190	
87 aaa gtg acc tgt gac atc cgg ctc cgg gtt cga gca gag tac tgc gag	624
88 Lys Val Thr Cys Asp Ile Arg Leu Arg Val Arg Ala Glu Tyr Cys Glu	
89 195 200 205	
91 cat ggg cca gcc ttg gag cag ggc gtg gca tcc cgg cgg ccc cag gcg	672
92 His Gly Pro Ala Leu Glu Gln Gly Val Ala Ser Arg Arg Pro Gln Ala	
93 210 215 220	
95 ctg gcg cgg cag ctg gac gtg ttt ggg cag gcc acc gca gtg ctg cgc	720
96 Leu Ala Arg Gln Leu Asp Val Phe Gly Gln Ala Thr Ala Val Leu Arg	
97 225 230 235 240	
99 tca agg gac ctg ggc tct gtg gtt tgt gac atc aag ttc tca gag ctc	768
100 Ser Arg Asp Leu Gly Ser Val Val Cys Asp Ile Lys Phe Ser Glu Leu	
101 245 250 255	
103 tcc tat ctg gac gcc ttc tgg ggc gac tac ctg agt ggc gcc ctg ctg	816
104 Ser Tyr Leu Asp Ala Phe Trp Gly Asp Tyr Leu Ser Gly Ala Leu Leu	
105 260 265 270	
107 cag gcc ctg cgg ggc gtg ttc ctg act gag gcc ctg cga gag gct gtg	864
108 Gln Ala Leu Arg Gly Val Phe Leu Thr Glu Ala Leu Arg Glu Ala Val	
109 275 280 285	
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112 Gly Arg Glu Ala Val Arg Leu Leu Val Ser Val Asp Glu Ala Asp	
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117 <211> LENGTH: 303	
118 <212> TYPE: PRT	
119 <213> ORGANISM: Homo sapiens	
121 <400> SEQUENCE: 2	
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127 Cys Leu Asp Tyr Tyr Gly Met Leu Ser Leu His Arg Met Phe Glu Val	
128 20 25 30	
131 Val Gly Gly Gln Leu Thr Glu Cys Glu Leu Glu Leu Ala Phe Leu	

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132	35	40	45	
135	Leu Asp Glu Ala Pro Gly Ala Ala Gly Gly Leu Ala Arg Ala Arg Ser			
136	50	55	60	
139	Gly Leu Glu Leu Leu Leu Glu Leu Glu Arg Arg Gly Gln Cys Gly Glu			
140	65	70	75	80
143	Ser Asn Leu Arg Leu Leu Gly Gln Leu Leu Arg Val Leu Ala Arg His			
144	85	90	95	
147	Asp Leu Leu Pro His Leu Ala Arg Lys Arg Arg Arg Pro Val Ser Pro			
148	100	105	110	
151	Glu Arg Tyr Ser Tyr Gly Thr Ser Ser Ser Ser Lys Arg Thr Glu Gly			
152	115	120	125	
155	Ser Cys Arg Arg Arg Gln Ser Ser Ser Ser Ala Asn Ser Gln Gln			
156	130	135	140	
159	Gly Gln Trp Glu Thr Gly Ser Pro Pro Thr Lys Arg Gln Arg Arg Ser			
160	145	150	155	160
163	Arg Gly Arg Pro Ser Gly Gly Ala Arg Arg Arg Arg Arg Gly Ala Pro			
164	165	170	175	
167	Ala Ala Pro Gln Gln Ser Glu Pro Ala Arg Pro Ser Ser Glu Gly			
168	180	185	190	
171	Lys Val Thr Cys Asp Ile Arg Leu Arg Val Arg Ala Glu Tyr Cys Glu			
172	195	200	205	
175	His Gly Pro Ala Leu Glu Gln Gly Val Ala Ser Arg Arg Pro Gln Ala			
176	210	215	220	
179	Leu Ala Arg Gln Leu Asp Val Phe Gly Gln Ala Thr Ala Val Leu Arg			
180	225	230	235	240
183	Ser Arg Asp Leu Gly Ser Val Val Cys Asp Ile Lys Phe Ser Glu Leu			
184	245	250	255	
187	Ser Tyr Leu Asp Ala Phe Trp Gly Asp Tyr Leu Ser Gly Ala Leu Leu			
188	260	265	270	
191	Gln Ala Leu Arg Gly Val Phe Leu Thr Glu Ala Leu Arg Glu Ala Val			
192	275	280	285	
195	Gly Arg Glu Ala Val Arg Leu Leu Val Ser Val Asp Glu Ala Asp			
196	290	295	300	
199	<210> SEQ ID NO: 3			
200	<211> LENGTH: 1883			
201	<212> TYPE: DNA			
202	<213> ORGANISM: Homo sapiens			
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205	<221> NAME/KEY: CDS			
206	<222> LOCATION: (124)..(1101)			
207	<223> OTHER INFORMATION:			
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213	aggagtcatc ggacgccaga atctggccgg gttctgagct tggccgcct ccctcccccg	120		
215	gga atg gcg cta tcc ggg tcg acc ccg gcc ccg tgc tgg gag gag gat	168		
216	Met Ala Leu Ser Gly Ser Thr Pro Ala Pro Cys Trp Glu Glu Asp			
217	1 5 10 15			
219	gag tgc ctg gac tac tac ggg atg ctg tcg ctt cac cgt atg ttc gag	216		
220	Glu Cys Leu Asp Tyr Tyr Gly Met Leu Ser Leu His Arg Met Phe Glu			

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223	gtg	gtg	ggc	264
224	Val	Val	Gly	Gly
225	35	40	45	
227	ctg	ctg	gat	gag
228	Leu	Leu	Asp	Glu
229	50	55	60	
231	agc	ggc	cta	gag
232	Ser	Gly	Leu	Glu
233	65	70	75	
235	gag	agc	aac	ctg
236	Glu	Ser	Asn	Leu
237	80	85	90	95
239	cac	gac	ctg	ctg
240	His	Asp	Leu	Leu
241	100	105	110	
243	cca	gaa	cgc	tat
244	Pro	Glu	Arg	Tyr
245	115	120	125	
247	ggt	agt	tgc	cgt
248	Gly	Ser	Cys	Arg
249	130	135	140	
251	cag	ggt	cag	tgg
252	Gln	Gly	Gln	Trp
253	145	150	155	
255	agt	cgg	ggc	ccc
256	Ser	Arg	Gly	Arg
257	160	165	170	175
259	cca	gcc	gca	ccc
260	Pro	Ala	Ala	Pro
261	180	185	190	
263	ggc	aaa	gtg	acc
264	Gly	Lys	Val	Thr
265	195	200	205	
267	gag	cat	ggg	cca
268	Glu	His	Gly	Pro
269	210	215	220	
271	gcg	ctg	gca	ggc
272	Ala	Leu	Ala	Arg
273	225	230	235	
275	cgc	tca	agg	gac
276	Arg	Ser	Arg	Asp
277	240	245	250	255
279	ctc	tcc	tat	ctg
280	Leu	Ser	Tyr	Leu
281	260	265	270	
283	ctg	cag	gcc	ctg
284	Leu	Gln	Ala	Leu
285	275	280	285	

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288	Val	Gly	Arg	Glu	Ala	Val	Arg	Leu	Leu	Val	Ser	Val	Asp	Glu	Ala	Asp	
289	290					295						300					
291	tat	gag	gct	ggc	cgg	cgc	cgc	ctg	ttg	ctg	atg	gag	gag	gaa	ggg	ggg	1080
292	Tyr	Glu	Ala	Gly	Arg	Arg	Arg	Leu	Leu	Leu	Met	Glu	Glu	Glu	Gly	Gly	
293	305					310					315						
295	cgg	cgc	ccg	aca	gag	gcc	tcc	tgatccagga	ctggcaggat	tgatcccacc							1131
296	Arg	Arg	Pro	Thr	Glu	Ala	Ser										
297	320					325											
299	tccaaagtctc	cgggccacact	tctccctggga	ggacgaccat	ctctaccct	tgacagcccc											1191
301	tcccacagga	tgtggctct	gaggcctaaa	ccatttccag	ctgagttcc	ttcccaagact											1251
303	cctcttaccc	ccagggtgtc	ccccttagcc	tccggaggcg	ggggctggc	ctgtatctca											1311
305	gaaggggaggg	gcacagctac	acactcacca	aaggcccccc	tgcacattgt	atctctgatc											1371
307	ttgggctgtc	tgcactgtca	caggtgcaca	cactcgctca	tgctcacact	gccctgtcg											1431
309	agatcttccc	tgggcctctg	ccctggcctg	cttcccagca	cacacttctt	tggcctaagg											1491
311	gtttctctct	caggacacct	aatttgcacca	caaccaacct	gggcttcage	cacatcagtg											1551
313	ggcactggag	ctggggtgca	catggggcct	gctcacctt	cccacacatc	tccagccagc											1611
315	cagggccctg	cccagcttca	attacagac	ctgactctcc	tcaccttccc	ccctgctgtc											1671
317	cagagctgaa	catagactt	gacttggatg	tcacctggag	tgtcacatgg	gagtgttatg											1731
319	gcagcatcat	accaaggcct	actgttgac	atggggccaa	aaccagtaaa	cagccacctt											1791
321	cttggaaagg	aatgcaaag	gctttggggg	tgatggaaaa	gacctttac	aaatgatacc											1851
323	aattaaactg	ccctggaaag	ggcataggtg	gg													1883
326	<210>	SEQ ID NO:	4														
327	<211>	LENGTH:	326														
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329	<213>	ORGANISM:	Homo sapiens														
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334	1				5				10			15					
337	Cys	Leu	Asp	Tyr	Tyr	Gly	Met	Leu	Ser	Leu	His	Arg	Met	Phe	Glu	Val	
338					20				25			30					
341	Val	Gly	Gly	Gln	Leu	Thr	Glu	Cys	Glu	Leu	Glu	Leu	Leu	Ala	Phe	Leu	
342					35				40			45					
345	Leu	Asp	Glu	Ala	Pro	Gly	Ala	Ala	Gly	Gly	Leu	Ala	Arg	Ala	Arg	Ser	
346					50				55			60					
349	Gly	Leu	Glu	Leu	Leu	Glu	Leu	Glu	Arg	Arg	Gly	Gln	Cys	Gly	Glu		
350					65				70			75			80		
353	Ser	Asn	Leu	Arg	Leu	Leu	Gly	Gln	Leu	Leu	Arg	Val	Leu	Ala	Arg	His	
354									85			90			95		
357	Asp	Leu	Leu	Pro	His	Leu	Ala	Arg	Lys	Arg	Arg	Arg	Pro	Val	Ser	Pro	
358									100			105			110		
361	Glu	Arg	Tyr	Ser	Tyr	Gly	Thr	Ser	Ser	Ser	Ser	Lys	Arg	Thr	Glu	Gly	
362									115			120			125		
365	Ser	Cys	Arg	Arg	Arg	Arg	Gln	Ser	Ser	Ser	Ser	Ala	Asn	Ser	Gln	Gln	
366									130			135			140		
369	Gly	Gln	Trp	Glu	Thr	Gly	Ser	Pro	Pro	Thr	Lys	Arg	Gln	Arg	Arg	Ser	
370									145			150			155		160
373	Arg	Gly	Arg	Pro	Ser	Gly	Gly	Ala	Arg	Arg	Arg	Arg	Arg	Gly	Ala	Pro	
374									165			170			175		

**VERIFICATION SUMMARY**

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L:14 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date